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**RAW SEQUENCE LISTING
PATENT APPLICATION US/09/945,182**

OIPE

DATE: 01/11/2002
TIME: 22:33:09

INPUT SET: S36718.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

1 SEQUENCE LISTING

(1) General Information:

5 (i) APPLICANT: Celeste, Anthony J.
6 Wozney, John
7 Rosen, Vicki A.
8 Wolfman, Neil
9 Thomsen, Gerald H.
10 Melton, Douglas A.

12 (i) TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS

14 (iii) NUMBER OF SEQUENCES: 35

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: GENETICS INSTITUTE, INC.
18 (B) STREET: 87 CambridgePark Drive
19 (C) CITY: Cambridge
20 (D) STATE: Massachusetts
21 (E) COUNTRY: USA
22 (F) ZIP: 02140

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk
26 (B) COMPUTER: IBM PC compatible
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

30- (vi) CURRENT APPLICATION DATA:

31 (A) APPLICATION NUMBER: 09/945,182

32 FILING DATE:

34

35 (vii) PRIOR APPLICATION DATA:
36 (A) APPLICATION NUMBER: 08/808,324

40 (viii) ATTORNEY/AGENT INFORMATION:

41 (A) NAME: Lazar, Steven R.
42 (B) REGISTRATION NUMBER: 32,618
43 (C) REFERENCE/DOCKET NUMBER: 5202-D

45 (ix) TELECOMMUNICATION INFORMATION:
46 (A) TELEPHONE: 617 498-8260

2.

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/945,182DATE: 01/11/2002
TIME: 22:33:09

INPUT SET: S36718.raw

47 (B) TELEFAX: 617 876-5851
4849
50 (2) INFORMATION FOR SEQ ID NO:1:
5152 (i) SEQUENCE CHARACTERISTICS:
53 (A) LENGTH: 926 base pairs
54 (B) TYPE: nucleic acid
55 (C) STRANDEDNESS: single
56 (D) TOPOLOGY: linear
5758 (ii) MOLECULE TYPE: DNA (genomic)
5960 (vi) ORIGINAL SOURCE:
61 (A) ORGANISM: Homo sapiens
6263 (vii) IMMEDIATE SOURCE:
64 (B) CLONE: v1-1
6566 (ix) FEATURE:
67 (A) NAME/KEY: mat_peptide
68 (B) LOCATION: 571..882
6970 (ix) FEATURE:
71 (A) NAME/KEY: CDS
72 (B) LOCATION: 1..882
7374 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
7576
77 GCG CGT AAT ACG ACT CAC TAT AGG GCG AAT TGG GTA CGG GGC CCA GGC
78 Ala Arg Asn Thr Thr His Tyr Arg Ala Asn Trp Val Arg Gly Pro Gly
79 -190 -185 -180 -175
80

48

81 AGC TGG ACT TCT CCG CCG TTG CTG CTG CTG TCC ACG TGC CCG GGC GCC
82 Ser Trp Thr Ser Pro Pro Leu Leu Leu Ser Thr Cys Pro Gly Ala
83 -170 -165 -160
84

96

85 GCC CGA GCG CCA CGC CTG CTG TAC TCG CGG GCA GCT GAG CCC CTA GTC
86 Ala Arg Ala Pro Arg Leu Leu Tyr Ser Arg Ala Ala Glu Pro Leu Val
87 -155 -150 -145
88

144

89 GGT CAG CGC TGG GAG GCG TTC GAC GTG GCG GAC GCC ATG AGG CGC CAC
90 Gly Gln Arg Trp Glu Ala Phe Asp Val Ala Asp Ala Met Arg Arg His
91 -140 -135 -130
92

192

93 CGT CGT GAA CCG CGC CCC CCC CGC GCG TTC TGC CTC TTG CTG CGC GCA
94 Arg Arg Glu Pro Arg Pro Pro Arg Ala Phe Cys Leu Leu Arg Ala
95 -125 -120 -115
96

240

97 GTG GCA GGC CCG GTG CCG AGC CCG TTG GCA CTG CGG CGA CTG GGC TTC
98 Val Ala Gly Pro Val Pro Ser Pro Leu Ala Leu Arg Arg Leu Gly Phe
99 -110 -105 -100 -95

288

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100	GGC TGG CCG GGC GGA GGG GGC TCT GCG GCA GAG GAG CGC GCG GTG CTA	336
101	Gly Trp Pro Gly Gly Gly Ser Ala Ala Glu Glu Arg Ala Val Leu	
102	-90	-85
103	-80	
104		
105	GTC GTC TCC TCC CGC ACG CAG AGG AAA GAG AGC TTA TTC CGG GAG ATC	384
106	Val Val Ser Ser Arg Thr Gln Arg Lys Glu Ser Leu Phe Arg Glu Ile	
107	-75	-70
108	-65	
109		
110	CGC GCC CAG GCC CGC GCG CTC GGG GCC GCT CTG GCC TCA GAG CCG CTG	432
111	Arg Ala Gln Ala Arg Ala Leu Gly Ala Ala Leu Ala Ser Glu Pro Leu	
112	-60	-55
113	-50	
114		
115	CCC GAC CCA GGA ACC GGC ACC GCG TCG CCA AGG GCA GTC ATT GGC GGC	480
116	Pro Asp Pro Gly Thr Gly Thr Ala Ser Pro Arg Ala Val Ile Gly Gly	
117	-45	-40
118	-35	
119		
120	CGC AGA CGG AGG AGG ACG GCG TTG GCC GGG ACG CGG ACA GCG CAG GGC	528
121	Arg Arg Arg Arg Arg Thr Ala Leu Ala Gly Thr Arg Thr Ala Gln Gly	
122	-30	-25
123	-20	-15
124		
125	CGC AGA CGG AGG AGG ACG GCG TTG GCC GGG ACG CGG ACA GCG CAG GGC	576
126	Ser Gly Gly Gly Ala Gly Arg Gly His Gly Arg Arg Gly Arg Ser Arg	
127	-10	-5
128	1	
129		
130	AGC GGC GGG GGC GCG GGC CGG GGC CAC GGG CGC AGG GGC CGG AGC CGC	624
131	Cys Ser Arg Lys Pro Leu His Val Asp Phe Lys Glu Leu Gly Trp Asp	
132	5	10
133	15	
134		
135		
136	TGC AGC CGC AAG CCG TTG CAC GTG GAC TTC AAG GAG CTC GGC TGG GAC	672
137	Cys Trp Ile Ile Ala Pro Leu Asp Tyr Glu Ala Tyr His Cys Glu Gly	
138	20	25
139	30	
140		
141	CTT TGC GAC TTC CCT TTG CGT TCG CAC CTC GAG GCG TAC CAC TGC GAG GGC	720
142	Leu Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala	
143	35	40
144	45	50
145		
146	ATC ATT CAG ACG CTG CTC AAC TCC ATG GCA CCA GAC GCG GCG CCG GCC	768
147	Ile Ile Gln Thr Leu Leu Asn Ser Met Ala Pro Asp Ala Ala Pro Ala	
148	55	60
149	65	
150		
151		
152		

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153 GCGGCCGAGG ATCC 926

154

155

156 (2) INFORMATION FOR SEQ ID NO:2:

157

158 (i) SEQUENCE CHARACTERISTICS:

159 (A) LENGTH: 294 amino acids

160 (B) TYPE: amino acid

161 (D) TOPOLOGY: linear

162

163 (ii) MOLECULE TYPE: protein

164

165 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

166

167 Ala Arg Asn Thr Thr His Tyr Arg Ala Asn Trp Val Arg Gly Pro Gly

168 -190 -185 -180 -175

169

170 Ser Trp Thr Ser Pro Pro Leu Leu Leu Ser Thr Cys Pro Gly Ala

171 -170 -165 -160

172

173 Ala Arg Ala Pro Arg Leu Leu Tyr Ser Arg Ala Ala Glu Pro Leu Val

174 -155 -150 -145

175

176 Gly Gln Arg Trp Glu Ala Phe Asp Val Ala Asp Ala Met Arg Arg His

177 -140 -135 -130

178

179 Arg Arg Glu Pro Arg Pro Pro Arg Ala Phe Cys Leu Leu Leu Arg Ala

180 -125 -120 -115

181

182 Val Ala Gly Pro Val Pro Ser Pro Leu Ala Leu Arg Arg Leu Gly Phe

183 -110 -105 -100 -95

184

185 Gly Trp Pro Gly Gly Ser Ala Ala Glu Glu Arg Ala Val Leu

186 -90 -85 -80

187

188 Val Val Ser Ser Arg Thr Gln Arg Lys Glu Ser Leu Phe Arg Glu Ile

189 -75 -70 -65

190

191 Arg Ala Gln Ala Arg Ala Leu Gly Ala Ala Leu Ala Ser Glu Pro Leu

192 -60 -55 -50

193

194 Pro Asp Pro Gly Thr Gly Thr Ala Ser Pro Arg Ala Val Ile Gly Gly

195 -45 -40 -35

196

197 Arg Arg Arg Arg Arg Thr Ala Leu Ala Gly Thr Arg Thr Ala Gln Gly

198 -30 -25 -20 -15

199

200 Ser Gly Gly Gly Ala Gly Arg Gly His Gly Arg Arg Gly Arg Ser Arg

201 -10 -5 1

202

203 Cys Ser Arg Lys Pro Leu His Val Asp Phe Lys Glu Leu Gly Trp Asp

204 5 10 15

205

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206 Asp Trp Ile Ile Ala Pro Leu Asp Tyr Glu Ala Tyr His Cys Glu Gly
207 20 25 30
208
209 Leu Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala
210 35 40 45 50
211
212 Ile Ile Gln Thr Leu Leu Asn Ser Met Ala Pro Asp Ala Ala Pro Ala
213 55 60 65
214
215 Ser Cys Cys Val Pro Ala Arg Leu Ser Pro Ile Ser Ile Leu Tyr Ile
216 70 75 80
217
218 Asp Ala Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val
219 85 90 95
220
221 Glu Ala Cys Gly Cys Arg
222 100
223
224 (2) INFORMATION FOR SEQ ID NO:3:
225
226 (i) SEQUENCE CHARACTERISTICS:
227 (A) LENGTH: 1207 base pairs
228 (B) TYPE: nucleic acid
229 (C) STRANDEDNESS: single
230 (D) TOPOLOGY: linear
231
232 (ii) MOLECULE TYPE: DNA (genomic)
233
234 (vi) ORIGINAL SOURCE:
235 (A) ORGANISM: Homo sapiens
236
237 (vii) IMMEDIATE SOURCE:
238 (B) CLONE: MP52
239
240 (ix) FEATURE:
241 (A) NAME/KEY: CDS
242 (B) LOCATION: 845..1204
243
244
245 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
246
247 ACCGGGCGGC CCTGAACCCA AGCCAGGACA CCCTCCCCAA ACAAGGCAGG CTACAGCCCG 60
248
249 GACTGTGACC CCAAAAGGAC AGCTTCCCGG AGGCAAGGCA CCCCCAAAAG CAGGATCTGT 120
250
251 CCCCAGCTCC TTCCTGCTGA AGAAGGCCAG GGAGCCGGG CCCCCACGAG AGCCAAGGA 180
252
253 GCCGTTTCGC CCACCCCCCA TCACACCCCA CGAGTACATG CTCTCGCTGT ACAGGACGCT 240
254
255 GTCCGATGCT GACAGAAAGG GAGGCAACAG CAGCGTGAAG TTGGAGGCTG GCCTGGCAA 300
256
257 CACCATCACC AGCTTTATTG ACAAAAGGGCA AGATGACCGA GGTCCCGTGG TCAGGAAGCA 360
258

ACCGGGCGGC CCTGAACCCA AGCCAGGACA CCCTCCCCAA ACAAGGCAGG CTACAGCCCG 60
GACTGTGACC CCAAAAGGAC AGCTTCCCGG AGGCAAGGCA CCCCCAAAAG CAGGATCTGT 120
CCCCAGCTCC TTCCTGCTGA AGAAGGCCAG GGAGCCGGG CCCCCACGAG AGCCAAGGA 180
GCCGTTTCGC CCACCCCCCA TCACACCCCA CGAGTACATG CTCTCGCTGT ACAGGACGCT 240
GTCCGATGCT GACAGAAAGG GAGGCAACAG CAGCGTGAAG TTGGAGGCTG GCCTGGCAA 300
CACCATCACC AGCTTTATTG ACAAAAGGGCA AGATGACCGA GGTCCCGTGG TCAGGAAGCA 360

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SEQUENCE VERIFICATION REPORT
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DATE: 01/11/2002
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Line

Error

Original Text

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**SEQUENCE MISSING ITEM REPORT
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<< THERE ARE NO ITEMS MISSING >>

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SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/09/945,182

DATE: 01/11/2002
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INPUT SET: S36718.raw

Line	Original Text	Corrected Text
1945	(C) INDIVIDUAL ISOLATE: primer number 8	(C) INDIVIDUAL ISOLATE: primer number 8